CECH et al. Application No.: 08/911,312 Page 17

Support for the Claim Amendments

Amendment of the sequence "W(L/I)XXXXhhXhh(Q/R)X

FFYXTEXXXXXXXXXX(F/Y)(F/Y)RXXXWXX(L/I)XXHXIXXXX(K/M) (SEQ ID NO:471)" on page 27, lines 5 and 6, and claim 96, page 216 (lines 3 and 4 of the claim), to --XFFYXTEXXXXXXXXX(F/Y)(F/Y)RXXXWXX(L/I)XXHXIXXXX(K/M)-- where the bolded and underlined "X" is deleted from position 29, finds support in the corresponding motif sequences represented by "Trp-R1-X7-R1-R1-R2-X-Phe-Phe-Tyr-X-Thr-Glu-X8-9-R3-R3-Arg-R4-X2-Trp (SEQ ID NOS:16 and 17)" (where R3 is Phe or Tyr), on page 26, lines 1 and 2; "W-X12-F-F-Y-X-T-E-X10-11-R-X3-W-X7-I (SEQ ID NOS:119 and 120)", on page 26, line 19; and, "W-L-X-Y-X-X-h-h-X-h-h-X-p-F-F-Y-X-T-E-X-p-X-X-X-y-X-X-Y-X-R-K-X-X-W (SEQ ID NO:473)", on page 26, line 21. In each of these motif sequences, the distance from the "Glu" or "E" in the subsequence "-Phe-Phe-Tyr-X-Thr-Glu-" or "-F-F-Y-X-T-E-" to the next "Arg or "R" is given as "-X8-9-R3-R3-", "-X10-11-", or "-X-p-X-X-X-p-X-X-Y-X-Y-X-", respectively. In each case, the number of amino acid residues separating these two amino acids is always 10 or 11 (not 12, as is found in the unamended sequence).

Support for the amendment to the sequence

"(L/I)L(R/K)(L/V)XDD(F/Y)Lh(I/V)(T/S) (SEQ ID NO:475)" (emphasis added), on page 27, line 24, (and claim 101, as amended in amendment to claims, submitted under separate cover), is found in the Motif C regions of Figures 41, 48, 55, and 57C. In each instance, the amino acids found four residues prior to the "DD" common to Motif C are either "L" (in three cases), or "M" (in one case). This can be compared and contrasted to the similar situations at amino acids 5, 3 and 2 residues prior to the common "DD" of Motif C, represented by "(L/I)", "(R/K)", and "(L/V)", respectively. Each figure shows three occurrences of the first residue in each pair, followed by one occurrence of the second residue in each pair. The addition of the "M" to the amended sequence at this position is consistent with this representation.

The deletion of the sentence on page 143, line 26 reflects the fact that no discernable characters in Figure 12 appear to be presented in **bold-face** type.

CECH et al. Application No.: 08/911,312

Page 18

The translation of "TGA" in standard usage is a "stop" codon, represented in the amino acid translations in Figure 12 by "×". In the Euploites aediculatus sequences of Figure 12, non-standard codon usage translates "TGA" as "Cys" or "C". In a few cases, however (SEQ ID NO:3, nucleotide positions 161-163 = SEQ ID NO:179, position 1; positions 706-708 = SEQ ID NO:163, position 48; and positions 1462-1464 = SEQ ID NO:172, position 11), "TGA" has been translated in Figure 12 by "×". For consistency, the Sequence Listing has included these three sequences in conformity to the non-standard codon usage, with these three positions coded by "Cys".

The amendment to page 155, lines 24-31, and page 156, lines 1-5, places the actual GenBank sequence for EST AA281296, given at residues 1679 to 2067 of SEQ ID NO:117, in the Specification where another sequence was inadvertently substituted. This amendment corrects an error of a typographical nature made without deceptive intent.

The amended sequence for SEQ ID NO:137 at page 177, line 1 and page 191, line 17, corrects a lower case "c" to an upper case "C", where altered nucleotides are in lower case, in the sequence "5'-TGCGCACGTGGGAAGCCCTGGCagatctgAatt

CcaCcATGCCGCGCTCCCCGCTG-3" (emphasis added). Support for this amendment may be found at all other occurrences of the exact sequence on page 177, lines 14 and 15, page 190, lines 10 and 11, and page 190, lines 18 and 19.

The amendment on page 181, line 1, to add the last two lines of amino acids to the fusion protein on page 180, lines 16-36 (SEQ ID NO:141), finds support on pages 166-167 in WO 98/14592, published April 9, 1998, from the parent application PCT/US97/17618, filed October 1, 1997, where the corresponding sequence in its entirety can be found. This amendment corrects an error of a typographical nature made without deceptive intent.

The amendment on page 198, line 1, corrects an error of a typographical nature made without deceptive intent. Support for this amendment can be found on page 250 in parent application PCT/US97/17885, filed October 1, 1997, which was published as WO 98/14593 on April 9, 1998, where the correct primer designation "hTR-445" appears.

CECH et al. Application No.: 08/911,312

Page 19

All other amendments pertain to assignment or correction of unique identifiers, explanation of sequence identifiers in Figures, or correction of typographical errors.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Petition for a waiver of Requirements under 37 C.F.R. §§ 1.821-1.825

Applicants are submitting a petition for a waiver of the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, 37 C.F.R. §§ 1.821-1.825, for an amino acid sequence found in the Specification of the instant application, under a separate cover.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at (415) 576-0200; or Ted Apple, Registration No. 36,429, at (650) 324-6370.

Respectfully submitted,

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